

1
SEQUENCE LISTING

RECEIVED

JUN 21 2001

TECH CENTER 1600/2900

B
S13
D12
<110> IMHOF, BEAT ALBET
AURRAND-LIONS, MICHEL

<120> VASCULAR ADHESION MOLECULES AND MODULATION OF THEIR
FUNCTION

<130> 11422/0264679

<140> 09/524,531

<141> 2000-03-13

<150> EP 99.200746.8

<151> 1999-03-11

<160> 21

<170> PatentIn Ver. 2.1

<210> 1

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> modified_base

<222> (6)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (10)..(12)

<223> a, t, c, g, other or unknown

<400> 1

tayagntgyn nngcytcyaa

20

<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> modified_base

<222> (10)..(12)

<223> a, t, c, g, other or unknown

<400> 2

taycrgtgyn nngcytcyaa

20



<210> 3
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 <223> Description of Artificial Sequence: primer

<220>
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 <222> (10)..(12)
 <223> a, t, c, g, other or unknown

<400> 3
 taytaytgyn nngcytcyaa

20

<210> 4
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 4
 gaggtacttg catgtgct

18

<210> 5
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 5
 cgacaggtgt cagataaca

19

<210> 6
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 6
 caccctcctc actcgt

16

<210> 7
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer used
for detection of JAM-2 transcript

<400> 7

gactcacaga caagtgac

18

<210> 8

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer used
for detection JAM-2 transcript

<400> 8

caccctcctc actcgt

16

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
Hprt cDNA

<400> 9

gttggataca ggccagactt tgttg

25

<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
Hprt cDNA

<400> 10

gagggtaggc tggcctatag gct

23

<210> 11

<211> 1943

<212> DNA

<213> Mus musculus

<400> 11

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ttacggactc acagacaagt gaccctagga ttgaatggaa gaaaatccaa gatggccaaa 240

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 tcttttaagg agttttctta aggaggctgg ctgaatattc ctttgttcaa aagaagtttt 1860
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 aattccaatc taaaaaaaaa aaa 1943

<210> 12

<211> 1631

<212> DNA

<213> Mus musculus

<400> 12

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 ggccagaaga cctgccccca cgacagtcgc tggagacacc ccagaccgga gagactgaca 240
 tcgggacagg acccgccctt ctgcttccac ctctcaggga cctcctctgc tccgccgccc 300
 ggcgaagtgc tgggagaccc agccgcctgt cgcgctcctg caggggggacc ctgagctagg 360
 cagccagctg gcgcccgcgt agatggcgag gagccccaa ggcctcctga tgctgctgct 420
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 agaccaccgt caagaagtca cagtaataga gttccaagag gctatttttg cttgtaaaaa 540
 cccaaagaag actacctctc ccagactgga gtggaagaag gtgggacagg ggggtctcctt 600
 ggtctactac caacaggctc tccaagggtg ctttaaagac cgtgctgaga tgatagattt 660
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 cgctccgact gagcaaggcc agaacctgca ggaagataaa gtcatgctag aagtactagt 780
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 aggggagttc atcagaagtt ttatgatctc taactcacia gaaatatttt aagcaaaacg 1440
 ttcttgccat cactaaatta caacctggca tcttgtgttg acctaaagga aatgtctggt 1500
 aatattctgg tttttgaagg caaatgaatg tcagtttgga gttgactata tcacactgac 1560
 tgtaaggcta atccaagaag caagaatata aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
 aaaaaaattt c 1631

<210> 13
 <211> 310
 <212> PRT
 <213> Mus musculus

<400> 13
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 His Phe Phe Leu Leu Leu Leu Phe Arg Gly Cys Met Ile Glu Ala Val
 20 25 30
 Asn Leu Lys Ser Ser Asn Arg Asn Pro Val Val His Glu Phe Glu Ser
 35 40 45
 Val Glu Leu Ser Cys Ile Ile Thr His Ser Gln Thr Ser Asp Pro Arg
 50 55 60
 Ile Glu Trp Lys Lys Ile Gln Asp Gly Gln Thr Thr Tyr Val Tyr Phe
 65 70 75 80
 Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly Arg Thr Asp Val Phe Gly
 85 90 95
 Lys Thr Ser Leu Arg Ile Trp Asn Val Thr Arg Ser Asp Ser Ala Ile
 100 105 110
 Tyr Arg Cys Glu Val Val Ala Leu Asn Asp Arg Lys Glu Val Asp Glu
 115 120 125
 Ile Thr Ile Glu Leu Ile Val Gln Val Lys Pro Val Thr Pro Val Cys
 130 135 140
 Arg Ile Pro Ala Ala Val Pro Val Gly Lys Thr Ala Thr Leu Gln Cys
 145 150 155 160
 Gln Glu Ser Glu Gly Tyr Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn
 165 170 175
 Asp Val Pro Leu Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Gln Asn
 180 185 190
 Ser Ser Phe His Val Asn Ser Glu Thr Gly Thr Leu Val Phe Asn Ala
 195 200 205
 Val His Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp
 210 215 220

Ala Gly Ala Ala Arg Cys Glu Gly Gln Asp Met Glu Val Tyr Asp Leu
225 230 235 240

Asn Ile Ala Gly Ile Ile Gly Gly Val Leu Val Val Leu Ile Val Leu
245 250 255

Ala Val Ile Thr Met Gly Ile Cys Cys Ala Tyr Arg Arg Gly Cys Phe
260 265 270

Ile Ser Ser Lys Gln Asp Gly Glu Ser Tyr Lys Ser Pro Gly Lys His
275 280 285

Asp Gly Val Asn Tyr Ile Arg Thr Ser Glu Glu Gly Asp Phe Arg His
290 295 300

Lys Ser Ser Phe Val Ile
305 310

<210> 14

<211> 298

<212> PRT

<213> Mus musculus

<400> 14

Met Ala Arg Ser Pro Gln Gly Leu Leu Met Leu Leu Leu Leu His Tyr
1 5 10 15

Leu Ile Val Ala Leu Asp Tyr His Lys Ala Asn Gly Phe Ser Ala Ser
20 25 30

Lys Asp His Arg Gln Glu Val Thr Val Ile Glu Phe Gln Glu Ala Ile
35 40 45

Leu Ala Cys Lys Thr Pro Lys Lys Thr Thr Ser Ser Arg Leu Glu Trp
50 55 60

Lys Lys Val Gly Gln Gly Val Ser Leu Val Tyr Tyr Gln Gln Ala Leu
65 70 75 80

Gln Gly Asp Phe Lys Asp Arg Ala Glu Met Ile Asp Phe Asn Ile Arg
85 90 95

Ile Lys Asn Val Thr Arg Ser Asp Ala Gly Glu Tyr Arg Cys Glu Val
100 105 110

Ser Ala Pro Thr Glu Gln Gly Gln Asn Leu Gln Glu Asp Lys Val Met
115 120 125

Leu Glu Val Leu Val Ala Pro Ala Val Pro Ala Cys Glu Val Pro Thr
130 135 140

Ser Val Met Thr Gly Ser Val Val Glu Leu Arg Cys Gln Asp Lys Glu
145 150 155 160

Gly Asn Pro Ala Pro Glu Tyr Ile Trp Phe Lys Asp Gly Thr Ser Leu
165 170 175

B1

Leu Gly Asn Pro Lys Gly Gly Thr His Asn Asn Ser Ser Tyr Thr Asn
180 185 190

Glu His Glu Ser Gly Ile Leu Gln Phe Asn Met Ile Ser Lys Met Asp
195 200 205

Ser Gly Glu Tyr Tyr Cys Glu Ala Arg Asn Ser Val Gly His Arg Arg
210 215 220

Cys Pro Gly Lys Arg Met Gln Val Asp Val Leu Asn Ile Ser Gly Ile
225 230 235 240

Ile Ala Thr Val Val Val Val Ala Phe Val Ile Ser Val Cys Gly Leu
245 250 255

Gly Thr Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
260 265 270

Phe Gln Lys Gly Ser Pro Ala Ser Lys Val Thr Thr Met Gly Glu Asn
275 280 285

Asp Phe Arg His Thr Lys Ser Phe Ile Ile
290 295

<210> 15

<211> 310

<212> PRT

<213> Homo sapiens

<400> 15

Met Ala Leu Arg Arg Pro Pro Arg Leu Arg Leu Cys Ala Arg Leu Pro
1 5 10 15

Asp Phe Phe Leu Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly Ala Val
20 25 30

Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu Phe Glu Ser
35 40 45

Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr Ser Asp Pro Arg
50 55 60

Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr Thr Tyr Val Phe Phe
65 70 75 80

Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly Arg Ala Glu Ile Leu Gly
85 90 95

Lys Thr Ser Leu Lys Ile Trp Asn Val Thr Arg Arg Asp Ser Ala Leu
100 105 110

Tyr Arg Cys Glu Val Val Ala Arg Asn Asp Arg Lys Glu Ile Asp Glu
115 120 125

Ile Val Ile Glu Leu Thr Val Gln Val Lys Pro Val Thr Pro Val Cys
 130 135 140
 Arg Val Pro Lys Ala Val Pro Val Gly Lys Met Ala Thr Leu His Cys
 145 150 155 160
 Gln Glu Ser Glu Gly His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn
 165 170 175
 Asp Val Pro Leu Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn
 180 185 190
 Ser Ser Phe His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala
 195 200 205
 Val His Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp
 210 215 220
 Ala Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
 225 230 235 240
 Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val Leu
 245 250 255
 Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly Tyr Phe
 260 265 270
 Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro Gly Lys Pro
 275 280 285
 Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly Asp Phe Arg His
 290 295 300
 Lys Ser Ser Phe Val Ile
 305 310

<210> 16
 <211> 212
 <212> PRT
 <213> Homo sapiens

<400> 16
 Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile Lys Asn Val Thr Arg
 1 5 10 15
 Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser Ala Pro Ala Glu Gln
 20 25 30
 Gly Gln Asn Leu Glu Asp Thr Val Thr Leu Glu Val Leu Val Ala Pro
 35 40 45
 Ala Val Pro Ser Cys Glu Val Pro Ser Ser Ala Leu Ser Gly Thr Val
 50 55 60
 Val Glu Leu Arg Cys Gln Asp Lys Glu Gly Asn Pro Ala Pro Glu Tyr
 65 70 75 80

Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu Glu Asn Pro Arg Leu Gly
85 90 95

Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met Asn Thr Lys Thr Gly Thr
100 105 110

Leu Gln Phe Asn Thr Val Ser Lys Leu Asp Thr Gly Glu Tyr Ser Cys
115 120 125

Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg Cys Pro Gly Lys Arg Met
130 135 140

Gln Val Asp Asp Leu Asn Ile Ser Gly Ile Ile Ala Ala Val Val Val
145 150 155 160

Val Ala Leu Val Ile Ser Val Cys Gly Leu Gly Val Cys Tyr Ala Gln
165 170 175

Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser Phe Gln Lys Ser Asn Ser
180 185 190

Ser Ser Lys Ala Thr Thr Met Ser Glu Asn Asp Phe Lys His Thr Lys
195 200 205

Ser Phe Ile Ile
210

<210> 17

<211> 1296

<212> DNA

<213> Homo sapiens

<400> 17

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ccagtggtag	aggaatttga	aagtgtggaa	ctgtcttgca	tcattacgga	ttcgcagaca	180
agtgacccca	ggatcgagtg	gaagaaaatt	caagatgaac	aaaccacata	tgtgtttttt	240
gacaacaaaa	ttcagggaga	cttggcgggt	cgtgcagaaa	tactggggaa	gacatccctg	300
aagatctgga	atgtgacacg	gagagactca	gccctttatc	gctgtgaggt	cgttgctcga	360
aatgaccgca	aggaaattga	tgagattgtg	atcgagttaa	ctgtgcaagt	gaagccagtg	420
accctgtct	gtagagtgcc	gaaggctgta	ccagtaggca	agatggcaac	actgcactgc	480
caggagagtg	agggccaccc	ccggcctcac	tacagctggg	atcgcaatga	tgtaccactg	540
cccacggatt	ccagagccaa	tcccagattt	cgcaattctt	ctttccactt	aaactctgaa	600
acaggcactt	tggtgttcac	tgctgttcac	aaggacgact	ctgggcagta	ctactgcatt	660
gcttccaatg	acgcaggctc	agccagggtg	gaggagcagg	agatggaagt	ctatgacctg	720
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tgaaaataag	gggtctttta	gagtttggtg	cgtaaaaccc	cccgttggg	ccttggaaac	1260
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<210> 18
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: sequence
 surrounding C-terminal cysteine of C2 domain
 (endothelial cell line t-end)

<220>

<221> MOD_RES

<222> (4)

<223> Any amino acid

<400> 18

Tyr Arg Cys Xaa Ala Ser
 1 5

<210> 19

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: sequence
 surrounding the C-terminal cysteine of C2 domain
 (endothelial cell line t-end)

<220>

<221> MOD_RES

<222> (4)

<223> Any amino acid

<400> 19

Tyr Gln Cys Xaa Ala Ser
 1 5

<210> 20

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: sequence
 surrounding the C-terminal cysteine of C2 domain
 (endothelial cell line t-end)

<220>

<221> MOD_RES

<222> (4)

<223> Any amino acid

<400> 20

Tyr Tyr Cys Xaa Ala Ser
1 5

<210> 21

<211> 300

<212> PRT

<213> Mus musculus

<400> 21

Met Gly Thr Glu Gly Lys Ala Gly Arg Lys Leu Leu Phe Leu Phe Thr
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20 25 30Ala Gln Ser Asp Val Gln Val Pro Glu Met Glu Ser Ile Lys Leu Thr
35 40 45Cys Thr Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe Val
50 55 60Gln Gly Ser Thr Thr Ala Leu Val Cys Tyr Asn Ser Gln Ile Thr Ala
65 70 75 80Pro Tyr Ala Asp Arg Val Thr Phe Ser Ser Glu Gly Ile Thr Phe Ser
85 90 95Ser Val Thr Arg Lys Asp Asn Gly Glu Tyr Thr Cys Met Val Ser Glu
100 105 110Glu Gly Gly Gln Asn Tyr Gly Glu Val Ser Ile His Leu Thr Val Leu
115 120 125Val Pro Pro Ser Lys Pro Thr Ile Ser Val Pro Ser Ser Val Thr Ile
130 135 140Gly Asn Arg Ala Val Leu Thr Cys Ser Glu His Asp Gly Ser Pro Pro
145 150 155 160Ser Glu Tyr Ser Trp Phe Lys Asp Gly Ile Ser Met Leu Thr Ala Asp
165 170 175Ala Lys Lys Thr Arg Ala Phe His Asn Ser Ser Phe Thr Ile Asp Pro
180 185 190Lys Ser Gly Asp Leu Tyr Phe Asp Phe Val Thr Ala Phe Asp Ser Gly
195 200 205Glu Tyr Tyr Cys Gln Ala Gln Asn Gly Tyr Gly Thr Ala Met Arg Ser
210 215 220Glu Ala Ala His Met Asp Ala Val Glu Leu Asn Val Gly Gly Ile Val
225 230 235 240Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Leu Leu Ile Phe Gly
245 250 255

Val Trp Phe Ala Tyr Ser Arg Gly Tyr Phe Glu Thr Thr Lys Lys Gly
260 265 270

Thr Ala Pro Gly Lys Lys Val Ile Tyr Ser Gln Pro Ser Thr Arg Ser
275 280 285

Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
290 295 300

B1
correl.
